

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/540,546
Source: JFwo
Date Processed by STIC: 11/27/06

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IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/540,546

DATE: 11/27/2006

TIME: 14:23:18

Input Set : A:\274130.Substitute.Sequence_Listing.TXT
 Output Set: N:\CRF4\11272006\J540546.raw

3 <110> APPLICANT: Fujisawa Pharmaceutical Co., Ltd.
 4 Matsuoka, Hideaki
 5 Fujimura, Takao
 6 Hayashi, Masako
 7 Aramori, Ichiro
 9 <120> TITLE OF INVENTION: New methods for selecting an immunosuppressive agent
 11 <130> FILE REFERENCE: 274130US0PCT
W--> 12 <140> CURRENT APPLICATION NUMBER: 10/540,546
 13 <141> CURRENT FILING DATE: 2005-06-24
 15 <150> PRIOR APPLICATION NUMBER: JP2002-378803
 16 <151> PRIOR FILING DATE: 2002-12-27
 18 <160> NUMBER OF SEQ ID NOS: 86
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 3255
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (1)..(3255)
 30 <223> OTHER INFORMATION: human histone deacetylase-4 (HDAC4) gene
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 34 Met Ser Ser Gln Ser His Pro Asp Gly Leu Ser Gly Arg Asp Gln Pro
 35 1 5 10 15
 37 gtg gag ctg ctg aat cct gcc cgc gtg aac cac atg ccc agc acg gtg 96
 38 Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val
 39 20 25 30
 41 gat gtg gcc acg gcg ctg cct ctg caa gtg gcc ccc tcg gca gtg ccc 144
 42 Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro
 43 35 40 45
 45 atg gac ctg cgc ctg gac cac cag ttc tca ctg cct gtg gca gag ccg 192
 46 Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro
 47 50 55 60
 49 gcc ctg cgg gag cag cag ctg cag cag gag ctc ctg gcg ctc aag cag 240
 50 Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln
 51 65 70 75 80
 53 aag cag cag atc cag agg cag atc ctc atc gct gag ttc cag agg cag 288
 54 Lys Gln Gln Ile Gln Arg Gln Ile Leu Ile Ala Glu Phe Gln Arg Gln
 55 85 90 95
 57 cac gag cag ctc tcc cgg cag cac gag gcg cag ctc cac gag cac atc 336
 58 His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile
 59 100 105 110

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61	aag	caa	caa	cag	gag	atg	ctg	gcc	atg	aag	cac	cac	cag	cag	ctg	ctg		384
62	Lys	Gln	Gln	Gln	Glu	Met	Leu	Ala	Met	Lys	Gln	Gln	Glu	Leu	Leu			
63	115								120						125			
65	gaa	cac	cag	cgg	aag	ctg	gag	agg	cac	cgc	cag	cag	cag	cag	ctg	gag		432
66	Glu	His	Gln	Arg	Lys	Leu	Glu	Arg	His	Arg	Gln	Glu	Gln	Glu	Leu	Glu		
67	130								135						140			
69	aag	cag	cac	cgg	qag	cag	aag	ctg	cag	cag	ctc	aag	aac	aag	gag	aag		480
70	Lys	Gln	His	Arg	Glu	Gln	Lys	Leu	Gln	Gln	Leu	Lys	Asn	Lys	Glu	Lys		
71	145								150				155		160			
73	ggc	aaa	gag	agt	gcc	gtg	gcc	agc	aca	gaa	gtg	aag	atg	aag	tta	caa		528
74	Gly	Lys	Glu	Ser	Ala	Val	Ala	Ser	Thr	Glu	Val	Lys	Met	Lys	Leu	Gln		
75	165								170						175			
77	gaa	ttt	gtc	ctc	aat	aaa	aag	aag	gcg	ctg	gcc	cac	cgg	aat	ctg	aac		576
78	Glu	Phe	Val	Leu	Asn	Lys	Lys	Lys	Ala	Leu	Ala	His	Arg	Asn	Leu	Asn		
79	180								185						190			
81	cac	tgc	att	tcc	agc	gac	cct	cgc	tac	tgg	tac	ggg	aaa	acg	cag	cac		624
82	His	Cys	Ile	Ser	Ser	Asp	Pro	Arg	Tyr	Trp	Tyr	Gly	Lys	Thr	Gln	His		
83	195								200				205					
85	agt	tcc	ctt	gac	cac	agt	tct	cca	ccc	cag	agc	gga	gtg	tcg	acc	tcc		572
86	Ser	Ser	Leu	Asp	Gln	Ser	Ser	Pro	Pro	Pro	Gln	Ser	Gly	Val	Ser	Thr	Ser	
87	210								215				220					
89	tat	aac	cac	ccg	gtc	ctg	gga	atg	tac	gac	gcc	aaa	gat	gac	ttc	cct		720
90	Tyr	Asn	His	Pro	Val	Leu	Gly	Met	Tyr	Asp	Ala	Lys	Asp	Asp	Phe	Pro		
91	225								230			235			240			
93	ctt	agg	aaa	aca	gct	tct	gaa	ccg	aat	ctg	aaa	tta	cgg	tcc	agg	cta		768
94	Leu	Arg	Lys	Thr	Ala	Ser	Glu	Pro	Asn	Leu	Lys	Leu	Arg	Ser	Arg	Leu		
95	245								250						255			
97	aag	cag	aaa	gtg	gcc	gaa	aga	cgg	agc	agc	ccc	ctg	tta	cgc	agg	aaa		816
98	Lys	Gln	Lys	Val	Ala	Glu	Arg	Arg	Ser	Ser	Pro	Leu	Leu	Arg	Arg	Lys		
99	260								265				270					
101	gac	ggg	cca	gtg	gtc	act	gct	cta	aaa	aag	cgt	ccg	ttg	gat	gtc	aca		864
102	Asp	Gly	Pro	Val	Val	Thr	Ala	Leu	Lys	Lys	Arg	Pro	Leu	Asp	Val	Thr		
103	275								280				285					
105	gac	tcc	gcg	tgc	agc	agc	gcc	cca	ggc	tcc	gga	ccc	agc	tca	ccc	aac		912
106	Asp	Ser	Ala	Cys	Ser	Ser	Ala	Pro	Gly	Ser	Gly	Pro	Ser	Ser	Pro	Asn		
107	290								295				300					
109	aac	agc	tcc	ggg	agc	gtc	agc	gcg	gag	aac	ggt	atc	gcg	ccc	gcc	gtc		960
110	Asn	Ser	Ser	Gly	Ser	Val	Ser	Ala	Glu	Asn	Gly	Ile	Ala	Pro	Ala	Val		
111	305								310			315			320			
113	ccc	agc	atc	ccg	gcg	gag	acg	agt	ttg	gcg	cac	aga	ctt	gtg	gca	cga		1008
114	Pro	Ser	Ile	Pro	Ala	Glu	Thr	Ser	Leu	Ala	His	Arg	Leu	Val	Ala	Arg		
115	325								330						335			
117	gaa	ggc	tcg	gcc	gct	cca	ctt	ccc	ctc	tac	aca	tcg	cca	tcc	ttg	ccc		1056
118	Glu	Gly	Ser	Ala	Ala	Pro	Leu	Pro	Leu	Tyr	Thr	Ser	Pro	Ser	Leu	Pro		
119	340								345				350					
121	aac	atc	acg	ctg	ggc	ctg	cct	gcc	acc	ggc	ccc	tct	gct	ggc	acg	gct		1104
122	Asn	Ile	Thr	Leu	Gly	Leu	Pro	Ala	Thr	Gly	Pro	Ser	Ala	Gly	Thr	Ala		
123	355								360				365					
125	ggc	cag	cag	gac	acc	gag	aga	ctc	acc	ctt	ccc	gcc	ctc	cag	cag	agg		1152

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126	Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg			
127	370	375	380	
129	ctc tcc ctt ttc ccc ggc acc cac ctc act ccc tac ctg agc acc tcg			1200
130	Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser			
131	385	390	395	400
133	ccc ttg gag cg gac gga ggg gca gca gcg cac agc cct ctt ctg cag cac			1248
134	Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His			
135	405	410	415	
137	atg gtc tta ctg gag cag cca ccg gca caa gca ccc ctc gtc aca ggc			1296
138	Met Val Leu Leu Glu Gln Pro Pro Ala Gln Ala Pro Leu Val Thr Gly			
139	420	425	430	
141	ctg gga gca ctg ccc ctc cac gca cag tcc ttg gtt ggt gca gac cgg			1344
142	Leu Gly Ala Leu Pro Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg			
143	435	440	445	
145	gtg tcc ccc tcc atc cac aag ctg cgg cag cac cgc cca ctg ggg cgg			1392
146	Val Ser Pro Ser Ile His Lys Leu Arg Gln His Arg Pro Leu Gly Arg			
147	450	455	460	
149	acc cag tcg gcc ccg ctg ccc cag aac gcc cag gct ctg cag cac ctg			1440
150	Thr Gln Ser Ala Frc Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu			
151	465	470	475	480
153	gtc atc cag cag cag cat cag cag ttt ctg gag aaa cac aag cag cag			1488
154	Val Ile Gln Gln His Gln Gln Phe Leu Glu Lys His Lys Gln Gln			
155	485	490	495	
157	tcc cag cag cag caa ctg cag atg aac aag atc atc ccc aag cca agc			1536
158	Phe Gln Gln Gln Leu Gln Met Asn Lys Ile Ile Pro Lys Pro Ser			
159	500	505	510	
161	gag cca gcc ccg cag ccg gag agc cac ccg gag gag acg gag gag gag			1584
162	Glu Pro Ala Arg Gln Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu			
163	515	520	525	
165	ctc cgt gag cac cag gct ctg ctg gac gag ccc tac ctg gac cgg ctg			1632
166	Leu Arg Glu His Gln Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu			
167	530	535	540	
169	ccg ggg cag aag gag gcg cac gca cag gcc ggc gtg cag gtg aag cag			1680
170	Pro Gly Gln Lys Glu Ala His Ala Gln Ala Gly Val Gln Val Lys Gln			
171	545	550	555	560
173	gag ccc att gag agc gat gag gaa gag gca gag ccc cca cgg gag gtg			1728
174	Glu Pro Ile Glu Ser Asp Glu Glu Ala Glu Pro Pro Arg Glu Val			
175	565	570	575	
177	gag ccg ggc cag cgc cag ccc agt gag cag gag ctg ctc ttc aga cag			1776
178	Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln			
179	580	585	590	
181	caa gcc ctc ctg ctg gag cag cag atc cac cag ctg agg aac tac			1824
182	Gln Ala Leu Leu Glu Gln Gln Arg Ile His Gln Leu Arg Asn Tyr			
183	595	600	605	
185	cag gcg tcc atg gag gcc ggc atc ccc gtg tcc ttc ggc ggc cac			1872
186	Gln Ala Ser Met Glu Ala Ala Gly Ile Pro Val Ser Phe Gly Gly His			
187	610	615	620	
189	agg cct ctg tcc ccg gcg cag tcc tca ccc gcg tct gcc acc ttc ccc			1920
190	Arg Pro Leu Ser Arg Ala Gln Ser Ser Pro Ala Ser Ala Thr Phe Pro			

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191	625	630	635	640	
193	gtg tct gtg cag gag ccc ccc acc aag ccg agg ttc acg aca ggc ctc				1968
194	Val Ser Val Gln Glu Pro Pro Thr Lys Pro Arg Phe Thr Thr Gly Leu				
195	645	650	655		
197	gtg tat gac acg ctg atg ctg aag cac cag tgc acc tgc ggg agt agc				2016
198	Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser				
199	660	665	670		
201	agc agc cac ccc gag cac gcc ggg agg atc cag agc atc tgg tcc cgc				2064
202	Ser Ser His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg				
203	675	680	685		
205	ctg cag gag acg ggc ctc cgg ggc aaa tgc gag tgc atc cgc gga cgc				2112
206	Leu Gln Glu Thr Gly Leu Arg Gly Lys Cys Glu Cys Ile Arg Gly Arg				
207	690	695	700		
209	aag gcc acc ctg gag gag cta cag acg gtg cac tcg gaa gcc cac acc				2160
210	Lys Ala Thr Leu Glu Glu Leu Gln Thr Val His Ser Glu Ala His Thr				
211	705	710	715	720	
213	ctc ctg tat ggc acg aac ccc ctc aac cgg cag aaa ctg gac agt aag				2208
214	Leu Leu Tyr Gly Thr Asn Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys				
215	725	730	735		
217	aaa ctt cta ggc tcg ctc gcc tcc gtg ttc gtc cgg ctc cct tgc ggt				2256
218	Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly				
219	740	745	750		
221	ggg gtt ggg gac agt gac acc ata tgg aac gag gtg cac tcg gcg				2304
222	Gly Val Gly Val Asp Ser Asp Thr Ile Trp Asn Glu Val His Ser Ala				
223	755	760	765		
225	ggg gca gcc cgc ctg gct gtg ggc tgc gtg gta gag ctg gtc ttc aag				2352
226	Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys				
227	770	775	780		
229	gtg gcc aca ggg gag ctg aag aat ggc ttt gct gtg gtc cgc ccc cct				2400
230	Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro				
231	785	790	795	800	
233	gga cac cat gcg gag gag agc acg ccc atg ggc ttt tgc tac ttc aac				2448
234	Gly His His Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn				
235	805	810	815		
237	tcc gtg gcc gtg gca gcc aag ctt ctg cag cag agg ttg agc gtg agc				2496
238	Ser Val Ala Val Ala Lys Leu Leu Gln Gln Arg Leu Ser Val Ser				
239	820	825	830		
241	aag atc ctc atc gtg gac tgg gac gtg cac cat gga aac ggg acc cag				2544
242	Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln				
243	835	840	845		
245	cag gct ttc tac agc gac cct agc gtc ctg tac atg tcc ctc cac cgc				2592
246	Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu His Arg				
247	850	855	860		
249	tac gac gat ggg aac ttc ttc cca ggc agc ggg gct cct gat gag gtg				2640
250	Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val				
251	865	870	875	880	
253	ggc aca ggg ccc ggc gtg ggt ttc aac gtc aac atg gct ttc acc ggc				2688
254	Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly				
255	885	890	895		

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257 ggc ctg gac ccc ccc atg gga gac gct gag tac ttg gcg gcc ttc aga	2736
258 Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg	
259 900 905 910	
261 acg gtg gtc atg ccg atc gcc agc gag ttt gcc ccg gat gtg gtg ctg	2784
262 Thr Val Val Met Pro Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu	
263 915 920 925	
265 gtg tca tca ggc ttc gat gcc gtg gag ggc cac ccc acc cct ctt ggg	2832
266 Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly	
267 930 935 940	
269 ggc tac aac ctc tcc gcc aga tgc ttc ggg tac ctg acg aag cag ctg	2880
270 Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu	
271 945 950 955 960	
273 atg ggc ctg gct ggc ggc cggtt gtc ctg gcc ctc gag gga ggc cac	2928
274 Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His	
275 965 970 975	
277 gac ctg acc gcc att tgc gac gcc tcg gaa gca tgt gtt tct gcc ttg	2976
278 Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu	
279 980 985 990	
281 ctg gga aac gag ctt gat ctc cca gaa aag gtt tta cag caa aga	3024
282 Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg	
283 995 1000 1005	
285 ccc aat gca aac gct gtc cgt tcc atg gag aaa gtc atg gag atc cac	3072
286 Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His	
287 1010 1015 1020	
289 agc aag tac tgg cgc tgc ctg cag cgc aca acc tcc aca gcg ggg cgt	3120
290 Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg	
291 1025 1030 1035 1040	
293 tct ctg atc gag gct cag act tgc gag aac gaa gaa gcc gag acg gtc	3168
294 Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val	
295 1045 1050 1055	
297 acc gcc atg gcc tcg ctg tcc gtg ggc gtg aag ccc gcc gaa aag aga	3216
298 Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg	
299 1060 1065 1070	
301 cca gat gag gag ccc atg gaa gag gag ccg ccc ctg tag	3255
302 Pro Asp Glu Glu Pro Met Glu Glu Pro Pro Leu	
303 1075 1080	
306 <210> SEQ ID NO: 2	
307 <211> LENGTH: 1084	
308 <212> TYPE: PRT	
309 <213> ORGANISM: Homo sapiens	
311 <400> SEQUENCE: 2	
312 Met Ser Ser Gln Ser His Pro Asp Gly Leu Ser Gly Arg Asp Gln Pro	
313 1 5 10 15	
315 Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val	
316 20 25 30	
318 Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro	
319 35 40 45	
321 Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro	
322 50 55 60	

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:24; N Pos. 4,5,6,7,8,9,12,56

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:60; Line(s) 4155
Seq#:61; Line(s) 4168
Seq#:62; Line(s) 4181
Seq#:63; Line(s) 4194
Seq#:66; Line(s) 4233
Seq#:67; Line(s) 4246
Seq#:68; Line(s) 4259
Seq#:69; Line(s) 4272
Seq#:74; Line(s) 4337
Seq#:75; Line(s) 4350
Seq#:76; Line(s) 4363
Seq#:77; Line(s) 4376

VERIFICATION SUMMARY

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Input Set : A:\274130.Substitute.Sequence_Listing.TXT
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L:12 M:283 W: Missing Blank Line separator, <140> field identifier
L:3600 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0